# RAW SEQUENCE LISTING
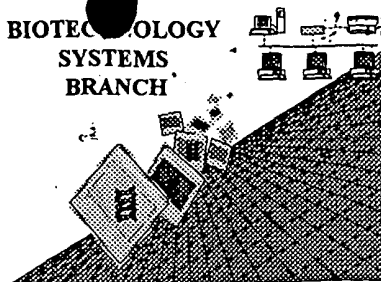# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: *09/665,308A*

Source: *OIPE*

Date Processed by STIC: *7/31/2001*

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**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY**
**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**


**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**
**PATENTIN 2.1 e-mail help:** patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
**PATENTIN 3.0 e-mail help:** patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:


## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
### http://www.uspto.gov/web/offices/pac/checker

**ERROR DETECTED**          **SUGGESTED CORRECTION**          SERIAL NUMBER: _09/665,308A_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos     was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
       prevent "wrapping."

· 2 _____ Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino     The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering     use space characters, instead.

4 _____ Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
       ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length .     Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
       each n or Xaa can only represent a single residue. Please present the maximum number of each
       residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"     sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
       previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
       the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
       Artificial or Unknown sequences.

7 _____ Skipped Sequences     Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
       (i)          SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
       (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
       This sequence is intentionally skipped

       Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences     Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
       (NEW RULES)     <210> sequence id number
       <400> sequence id number
       000

9 _____ Use of n's or Xaa's     Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
       In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
       Response     scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
       is Artificial Sequence

11 _____ Use of <220>     Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
       Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
       "Unknown." Please explain source of genetic material in <220> to <223> section.
       (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"     resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
       listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n     n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
       any value not specifically a nucleotide.

OIPE

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

*pp 1-3*

```
 3 <110> APPLICANT: Cahoon, Rebecca E.
 4        Klein, Theodore M.
 5        Odell, Joan T.
 6        Orozco, Emil M. Jr.
 8 <120> TITLE OF INVENTION: PLANT CELL CYCLIN GENES
10 <130> FILE REFERENCE: BB1149 US NA
12 <140> CURRENT APPLICATION NUMBER: US/09/665,308A
12 <141> CURRENT FILING DATE: 2000-09-19
12 <150> PRIOR APPLICATION NUMBER: 60/078,735
13 <151> PRIOR FILING DATE: 1998 March 20  1998-03-20   use this date format
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/06047
16 <151> PRIOR FILING DATE: 1999 March 19  1999-03-19
18 <160> NUMBER OF SEQ ID NOS: 32
20 <170> SOFTWARE: MICROSOFT OFFICE 97


RRORED SEQUENCES

1053 <210> SEQ ID NO: 21
1054 <211> LENGTH: 789
1055 <212> TYPE: DNA
1056 <213> ORGANISM: Triticum aestivum
1058 <400> SEQUENCE: 21
1059 cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat  60
1060 ctcaccgcct cgaccaaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120
1061 aaagtgatgg agcttttggt cttcagcacc ttgaaatgga ggatgcaagc tgttactgct 180
1062 tgctcgttta ttgactactt cctttgcaaa ttcaatgatc atgacacacc ctccatgctt 240
1063 gcattctcct gctcaactga cctcatcctg agcacaacta agtgagctga ttttttggtg 300
1064 ttcagacatt cagagattgc tggaagtgtt gcacttcctt catttgggga gcacaagact 360
1065 tcagttgtcg aaatggctac aactaattgc aagtatataa acaagggagt gtgatgtgac 420
1066 aggaaagatc ctgatgaagt gcttccttta tggaatgcct atctgaagtt tggactaaga 480
1067 gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540
1068 atgtttttat tgtagattag gatatgtgtg ttctgccacc ggttcgactt ctcatattag 600
1069 aaggcaagca gttagttcat atcttactac tttgcactat tgtagatgga tggtgaggga 660
1070 ttgagaggct actactatta atgtgcgtaa actttgcatc tttagctctc taaatgaaac 720
1071 cggtgatggt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780
1072 aaaaaaaaa                                        789 <- insert
1125 <210> SEQ ID NO: 23
1126 <211> LENGTH: 603  1132 (p. 2)
1127 <212> TYPE: DNA
1128 <213> ORGANISM: Zea mays
1130 <220> FEATURE:
1131 <221> NAME/KEY: unsure
1132 <222> LOCATION: (441)
1134 <220> FEATURE:
1135 <221> NAME/KEY: unsure
1136 <222> LOCATION: (447)
```

RAW SEQUENCE LISTING                    DATE: 07/31/2001
PATENT APPLICATION:  US/09/665,308A     TIME: 14:45:58

        Input Set : A:\BB1149USNA Corrected Seq List.txt
        Output Set: N:\CRF3\07312001\I665308A.raw

```
1138 <220> FEATURE:
1139 <221> NAME/KEY: unsure
1140 <222> LOCATION: (485)
1142 <220> FEATURE:
1143 <221> NAME/KEY: unsure
1144 <222> LOCATION: (498)
1146 <220> FEATURE:
1147 <221> NAME/KEY: unsure
1148 <222> LOCATION: (528)
1150 <220> FEATURE:
1151 <221> NAME/KEY: unsure
1152 <222> LOCATION: (553)
1154 <220> FEATURE:
1155 <221> NAME/KEY: unsure
1156 <222> LOCATION: (560)
1158 <220> FEATURE:
1159 <221> NAME/KEY: unsure
1160 <222> LOCATION: (576)..(577)
1162 <220> FEATURE:
1163 <221> NAME/KEY: unsure
1164 <222> LOCATION: (598)
1166 <400> SEQUENCE: 23
1167 aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggctaggct   60
1168 tctccgcgct caccgccgcg ctcgccgccg cctacctcga ccgctgcttc ctccccgggg  120
1169 gcgcgctccg gctcggcgac cagccctgga tggcgcgcct agccgccgtc acctgcttcg  180
1170 cgctcgccgc caaggtcgag gagacgcgcg tgccgccgct cctcgacctc cagctctacg  240
1171 ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc  300
1172 tgctcgtgct ctccgcgctt gggtggcgga tgcaccctgt cacgcccttc tcctacctcc  360
1173 agcccgtcct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgtc ctgctcgcgg  420
1174 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggccgcc gccgcgttgc  480
1175 tgatcacagc cgccgccggc gacggcggcg acggcgacgg cgacacggag ctcctggcgc  540
1176 tcatcaatgc ccccgaggac aagaccgccg agtgtgccaa gatcatctcc gaggtgacgg  600
1177 gcatgagctt cctcgcctgc gatgtcggcg tgagcgccgg aaataagcgt aagcacgcgg  660
1178 cggcgcagtt gtactcgccg ccgccgagcc cgagcggcgt gatcggcgcg ctgtcctgct  720
1179 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtgggcgc  780
1180 cgtcggcgtc cgtgtccgtg tcgtcctctc cagagccacc aggtcgggcc cccaagcgcg  840
1181 cagcggcggc gtcggcgtcg gcgtcggcgt cagccggggt cgcgccaccg gtccaggtcc  900
1182 cgcatcagct accccccgac gaggagagcc gcgacgcctg gccgtccacc tgcgccgcgt  960
1183 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcggtggc ggtggagaat 1020
1184 ggagaacaag gagcatcatt ggctcgcgtc ggtgagcagg agaacgaact attttgccca 1080
1185 ttgccgtgac agatggggggg tgttcactgc gtggagccgc gctgancaat ga         1132
1606 <210> SEQ ID NO: 32
1607 <211> LENGTH: 373
1608 <212> TYPE: PRT
1609 <213> ORGANISM: Nicotiana tabacum
1611 <400> SEQUENCE: 32
1612 Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu
1613  1               5                  10                  15
1615 Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Lys Trp Gly Asp Leu
```

*see item 9 on Erro Summary Sheet*

p.3

RAW SEQUENCE LISTING                    DATE: 07/31/2001
PATENT APPLICATION:   US/09/665,308A    TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

```
 1616              20                25                30
 1618 Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr
 1619          35                40                45
 1621 Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu
 1622      50                55                60
 1624 Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe
 1625 65                70                75                80
 1627 Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp
 1628              85                90                95
 1630 Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys
 1631          100               105               110
 1633 Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile
 1634          115               120               125
 1636 Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys
 1637      130               135               140
 1639 Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala
 1640 145               150               155               160
 1642 Lys Val Glu Glu Thr Gln Val Pro Leu Leu Leu Asp Phe Gln Val Glu
 1643          165               170               175
 1645 Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu
 1646          180               185               190
 1648 Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu
 1649          195               200               205
 1651 Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile
 1652      210               215               220
 1654 His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met
 1655 225               230               235               240
 1657 Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala
 1658          245               250               255
 1660 Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp
 1661          260               265               270
 1663 Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val
 1664      275               280               285
 1666 Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser
 1667      290               295               300
 1669 His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile
 1670 305               310               315               320
 1672 Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu
 1673          325               330               335
 1675 Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu
 1676          340               345               350
 1678 Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala
 1679          355               360               365
 1681 Val Gly Ser Pro His
 1682      370
->1685 (6
```

delete

—)

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

**VERIFICATION SUMMARY**                    DATE: 07/31/2001
PATENT APPLICATION:  US/09/665,308A         TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:156 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:157 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:159 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:161 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:162 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:163 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:204 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:207 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:213 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:291 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:293 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:294 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:295 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:388 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:442 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:466 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:761 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:762 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:786 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
```

VERIFICATION SUMMARY                    DATE: 07/31/2001
PATENT APPLICATION:  US/09/665,308A     TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

```
L:807 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:809 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1005 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1006 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1008 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1010 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1011 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1038 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1050 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1072 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:789 SEQ:21
L:1095 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1116 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1185 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1185 M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:1132 SEQ:23
L:1283 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1284 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1330 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1333 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1336 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1685 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
```